

OIKE

2

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/930,871

TIME: 17:11:13

Input Set : A:\LEX-0216-USA SEQLIST.txt

Output Set: N:\CRF3\08162001\I930871.raw

ENTERED

4 <110> APPLICANT: Turner, C. Alexander Jr.

5 Mathur, Daniel

6 Mathur, Brian

8 <120> TITLE OF INVENTION: Novel Human Ion Channel Proteins and Polynucleotides

Encoding the

9 Same

11 <130> FILE REFERENCE: LEX-0216-USA

OK C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/930,871

C--> 13 <141> CURRENT FILING DATE: 2001-08-14

13 <150> PRIOR APPLICATION NUMBER: US 60/225,989

14 <151> PRIOR FILING DATE: 2000-08-16

16 <160> NUMBER OF SEQ ID NOS: 20

18 <170> SOFTWARE: FastSEQ for Windows Version 4.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 5997

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <400> SEQUENCE: 1

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28	aaaaaagatg	acgacgaaaa	tggcccaaa	ccaaatagtg	acttggaagc	tggaaagAAC	180
29	cttccattta	tttatggaga	cattcctcca	gagatggtgt	cagagcccct	ggaggacctg	240
30	gacccctact	atatcaataa	gaaaactttt	atagtattga	ataaaggga	ggccatcttc	300
31	cgggttcagt	ccacctctgc	cctgtacatt	ttaactccct	tcaatcctct	taggaaaata	360
32	gctattaaga	ttttggtaca	ttcattatct	agcatgctaa	ttatgtgcac	tattttgaca	420
33	aactgtgtgt	ttatgacaat	gagtaaccct	cctgattgga	caaagaatgt	agaatacacc	480
34	ttcacaggaa	tataactttt	tgaatcactt	ataaaaatta	ttgcaagggg	attctgttta	540
35	gaagatttta	ctttccttcg	ggatccatgg	aactggctcg	atttactgt	cattacattt	600
36	gcgtacgtca	cagagtttgt	ggacctgggc	aatgtctcgg	cattgagaac	attcagagtt	660
37	ctccgagcat	tgaagacgat	ttcagtcatt	ccaggcctga	aaaccattgt	gggagccctg	720
38	atccagtcct	tgaagaagct	ctcagatgta	atgatcctga	ctgtgttctg	tctgagcgta	780
39	tttgccttaa	ttgggctgca	gctgttcatt	ggcaacctga	ggaataaatg	tatacaatgg	840
40	cctcccacca	atgcttccct	ggaggaacat	agtatagaaa	agaatataac	tgtgaattat	900
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42	tcaagatata	attatttccct	ggagggtttt	ttagatgcac	tactatgtgg	aaatagctct	1020
43	gatgcaggcc	aatgtccaga	gggatatatg	tgtgtgaaag	ctggtagaaa	tccaattat	1080
44	ggctacacaa	gctttgatac	cttcagttgg	gcttttttgt	ccttgtttcg	actaatgact	1140
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46	atattttttg	tgttggtcat	tttcttgggc	tcattctacc	taataaattt	gacctgggct	1260
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p. 5

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56	aacgagagcc	gtagagattc	cttgtttgtg	ccccgacgac	acggagagag	acgcaacagc	1860
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58	atgcacagca	ctgtggattg	caatgggtgtg	gtttccttgg	ttgggtggacc	ttcagttcct	1980
59	acatgcctg	ttggacagct	tctgccagag	ggaacaacca	ctgaaactga	aatgagaaag	2040
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61	cgagcaatga	gtatagccag	cattctaaca	aatacagtag	aagaacttga	agaatccagg	2160
62	cagaaatgcc	cacctgtgtg	gtataaattt	tccaacatat	tcttaatctg	ggactgttct	2220
63	ccatattggt	taaaagtga	acatgttgtc	aacctggttg	tgatggaccc	atttgttgac	2280
64	ctggccatca	ccatctgtat	tgtcttaaat	actcttttca	tggccatgga	gcactatcca	2340
65	atgacggacc	atttcaataa	tgtgcttaca	gtaggaaact	tggttttcac	tgggatcttt	2400
66	acagcagaaa	tgtttctgaa	aattattgcc	atggatcctt	actattattt	ccaagaaggc	2460
67	tggaatatct	ttgacggttt	tattgtgacg	cttagcctgg	tagaacttgg	actcgccaat	2520
68	gtggaaggat	tatctgttct	cgttcattt	cgattgtcga	gagttttcaa	gttggcaaaa	2580
69	tcttggccaa	cgttaaatat	gctaataaag	atcatcgcca	attccgtggg	ggctctggga	2640
70	aattttaacc	tcgtcttggc	catcatcgtc	ttcatttttg	ccgtggtcgg	catgcagctc	2700
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76	ctccaaattg	ctgtggatag	gatgcacaaa	ggagtagctt	atgtgaaaag	aaaaatatat	3060
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78	gatgatctaa	acaacaagaa	agacagttgt	atgtccaatc	atacarcaga	aattgggaaa	3180
79	gatcttgact	atcttaaaaga	tgtaaatgga	actacaagtg	gtataggaac	tggcagcagt	3240
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103	tgtcttaaca	tggtcacaat	gatggtggaa	acagatgacc	agagtgaata	tgtgactacc	4680
104	attttgtcac	gcatcaatct	ggtgttcatt	gtgctattta	ctggagagtg	tgtactgaaa	4740

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105 ctcatctctc tacgccatta ttattttacc attggatgga atatttttga ttttgtggtt 4800
106 gtcattctct ccattgtagg tatgtttctt gccgagctga tagaaaagta tttcgtgtcc 4860
107 cctaccctgt tccgagtgat ccgtcttgct aggattggcc gaatcctacg tctgatcaaa 4920
108 ggagcaaagg ggatccgcac gctgctcttt gctttgatga tgtcccttcc tgcgttggtt 4980
109 aacatcggcc tctactctt cctagtcagt ttcactctacg ccatctttgg gatgtccaac 5040
110 tttgcctatg ttaagaggga agttgggacg gatgacatgt tcaactttga gacctttggc 5100
111 aacagcatga tctgcctatt ccaaattaca acctctgctg gctgggatgg attgctagca 5160
112 cccattctca acagtaagcc acccgactgt gaccctaata aagttaacct tggaagctca 5220
113 gttaaggagg actgtgggaa cccatctgtt ggaattttct tttttgtcag ttacatcatc 5280
114 atatccttcc tgggtgtggt gaacatgtac atcgcggtca tcctggagaa cttcagtgtt 5340
115 gctactgaag aaagtgcaga gcctctgagt gaggatgact ttgagatgtt ctatgaggtt 5400
116 tgggagaagt ttgatcccgga tgcaactcag ttcatggaat ttgaaaaatt atctcagttt 5460
117 gcagctgcgc ttgaaccgcc tctcaatctg ccacaaccaa acaaaactcca gctcattgcc 5520
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119 acaaagcggg ttctaggaga gagtggagag atggatgctc tacgaatata gatggaagag 5640
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121 cgaaaacaag aggaagtatc tgctgtcatt attcagcgtg cttacagacg ccacctttta 5760
122 aagcgaactg taaaacaagc ttcttttacg tacaataaaa acaaaatcaa aggtggggct 5820
123 aatcttctta taaaagaaga catgataatt gacagaataa atgaaaactc tattacagaa 5880
124 aaaactgacg tgaccatgtc cactgcagct tgtccacctt cctatgaccg ggtgacaaag 5940
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129 <210> SEQ ID NO: 2

130 <211> LENGTH: 1998

131 <212> TYPE: PRT

132 <213> ORGANISM: homo sapiens

134 <220> FEATURE:

135 <221> NAME/KEY: VARIANT

136 <222> LOCATION: (1)...(1998)

137 <223> OTHER INFORMATION: Xaa = Any Amino Acid

139 <400> SEQUENCE: 2

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141 1 5 10 15
142 Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Arg Arg Ile Ala Glu Glu
143 20 25 30
144 Lys Ala Lys Asn Pro Lys Pro Asp Lys Lys Asp Asp Asp Glu Asn Gly
145 35 40 45
146 Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Asn Leu Pro Phe Ile
147 50 55 60
148 Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Glu Pro Leu Glu Asp Leu
149 65 70 75 80
150 Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys Gly
151 85 90 95
152 Lys Ala Ile Phe Arg Phe Ser Ala Thr Ser Ala Leu Tyr Ile Leu Thr
153 100 105 110
154 Pro Phe Asn Pro Leu Arg Lys Ile Ala Ile Lys Ile Leu Val His Ser
155 115 120 125
156 Leu Phe Ser Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe
157 130 135 140
158 Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr Thr

```

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159 145          150          155          160
160 Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Ile Ala Arg
161          165          170          175
162 Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp
163          180          185          190
164 Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val Asp
165          195          200          205
166 Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu
167          210          215          220
168 Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala Leu
169 225          230          235          240
170 Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val Phe
171          245          250          255
172 Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly Asn
173          260          265          270
174 Leu Arg Asn Lys Cys Ile Gln Trp Pro Pro Thr Asn Ala Ser Leu Glu
175          275          280          285
176 Glu His Ser Ile Glu Lys Asn Ile Thr Val Asn Tyr Asn Gly Thr Leu
177          290          295          300
178 Ile Asn Glu Thr Val Phe Glu Phe Asp Trp Lys Ser Tyr Ile Gln Asp
179 305          310          315          320
180 Ser Arg Tyr His Tyr Phe Leu Glu Gly Phe Leu Asp Ala Leu Leu Cys
181          325          330          335
182 Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Met Cys Val
183          340          345          350
184 Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp Thr Phe
185          355          360          365
186 Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Phe Trp
187          370          375          380
188 Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr Tyr Met
189 385          390          395          400
190 Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Ile Asn
191          405          410          415
192 Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn Gln Ala
193          420          425          430
194 Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln Met Ile
195          435          440          445
196 Glu Gln Leu Lys Lys Gln Gln Glu Ala Ala Gln Gln Ala Ala Thr Ala
197          450          455          460
198 Thr Ala Ser Glu His Ser Arg Glu Pro Ser Ala Ala Gly Arg Leu Ser
199 465          470          475          480
200 Asp Ser Ser Ser Glu Ala Ser Lys Leu Ser Ser Lys Ser Ala Lys Glu
201          485          490          495
202 Arg Arg Asn Arg Arg Lys Lys Arg Lys Gln Lys Glu Gln Ser Gly Gly
203          500          505          510
204 Glu Glu Lys Asp Glu Asp Glu Phe Gln Lys Ser Glu Ser Glu Asp Ser
205          515          520          525
206 Ile Arg Arg Lys Gly Phe Arg Phe Ser Ile Glu Gly Asn Arg Leu Thr
207          530          535          540

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208 Tyr Glu Lys Arg Tyr Ser Ser Pro His Gln Ser Leu Leu Ser Ile Arg
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210 Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Thr Ser Leu Phe Ser
211                               565                               570                               575
212 Phe Arg Gly Arg Ala Lys Asp Val Gly Ser Glu Asn Asp Phe Ala Asp
213                               580                               585                               590
214 Asp Glu His Ser Thr Phe Glu Asp Asn Glu Ser Arg Arg Asp Ser Leu
215                               595                               600                               605
216 Phe Val Pro Arg Arg His Gly Glu Arg Arg Asn Ser Asn Leu Ser Gln
217                               610                               615                               620
218 Thr Ser Arg Ser Ser Arg Met Leu Ala Val Phe Pro Ala Asn Gly Lys
219 625                               630                               635                               640
220 Met His Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Val Gly Gly
221                               645                               650                               655
222 Pro Ser Val Pro Thr Ser Pro Val Gly Gln Leu Leu Pro Glu Gly Thr
223                               660                               665                               670
224 Thr Thr Glu Thr Glu Met Arg Lys Arg Arg Ser Ser Ser Phe His Val
225                               675                               680                               685
226 Ser Met Asp Phe Leu Glu Asp Pro Ser Gln Arg Gln Arg Ala Met Ser
227                               690                               695                               700
228 Ile Ala Ser Ile Leu Thr Asn Thr Val Glu Glu Leu Glu Glu Ser Arg
229 705                               710                               715                               720
230 Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ser Asn Ile Phe Leu Ile
231                               725                               730                               735
232 Trp Asp Cys Ser Pro Tyr Trp Leu Lys Val Lys His Val Val Asn Leu
233                               740                               745                               750
234 Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys Ile Val
235                               755                               760                               765
236 Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr Asp His
237                               770                               775                               780
238 Phe Asn Asn Val Leu Thr Val Gly Asn Leu Val Phe Thr Gly Ile Phe
239 785                               790                               795                               800
240 Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr Tyr Tyr
241                               805                               810                               815
242 Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Thr Leu Ser
243                               820                               825                               830
244 Leu Val Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val Leu Arg
245                               835                               840                               845
246 Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr
247                               850                               855                               860
248 Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly
249 865                               870                               875                               880
250 Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala Val Val
251                               885                               890                               895
252 Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Asp Cys Val Cys Lys Ile
253                               900                               905                               910
254 Ala Ser Asp Cys Gln Leu Pro Arg Trp His Met Asn Asp Phe Phe His
255                               915                               920                               925
256 Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile Glu Thr

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:2172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:2182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:2512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:2522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:2783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:3046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:3056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20